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F1632 H10
10-30-01
PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/763,712A

DATE: 07/05/2001

TIME: 10:42:51

Input Set : A:\37157SEQ.txt

Output Set : N:\CRF3\07052001\I763712A.raw

OCT 12 2001

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ENTERED

3 <110> APPLICANT: Wakamiya, N.
5 <120> TITLE OF INVENTION: Novel Collectin
7 <130> FILE REFERENCE: 19036/37157
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/763,712A
C--> 9 <141> CURRENT FILING DATE: 2001-05-04
9 <150> PRIOR APPLICATION NUMBER: JP HEI 10-237611
10 <151> PRIOR FILING DATE: 1998-08-24
12 <160> NUMBER OF SEQ ID NOS: 32
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 2024
16 <212> TYPE: DNA
17 <213> ORGANISM: Homo Sapiens
19 <220> FEATURE:
20 <221> NAME/KEY: CDS
21 <222> LOCATION: (670)..(1695)
23 <400> SEQUENCE: 1
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26 aacctcatca cgaatctgca gcggtctgtg gatgacacaa gccaggctat ccagcgaatc 180
27 aagaacgact ttcaaaatct gcagcaggtt tttcttcaag ccaagaagga cacggattgg 240
28 ctgaaggaga aagtgcagag cttgcagacg ctggctgcca acaactctgc gttggccaaa 300
29 gccacaacg acacctgga ggatatgaac agccagctca actcattcac aggtcagatg 360
30 gagaacatca ccactatctc tcaagccaac gaggagaacc tgaaagacct gcaggactta 420
31 cacaaagatg cagagaatag aacagccatc aagttcaacc aactggagga acgcttccag 480
32 ctctttgaga cggatattgt gaacatcatt agcaatatca gttacacagc ccaccacctg 540
33 cggacgctga ccagcaatct aatgaagtc aggaccactt gcacagatac ccttaccaaa 600
34 cacacagatg atctgacctc cttgaataat accctggcca acatccgttt ggattctgtt 660
35 tctctcagg atg caa caa gat ttg atg agg tcg agg tta gac act gaa gta 711
36 Met Gln Gln Asp Leu Met Arg Ser Arg Leu Asp Thr Glu Val
37 1 5 10
38 gcc aac tta tca gtg att atg gaa gaa atg aag cta gta gac tcc aag 759
39 Ala Asn Leu Ser Val Ile Met Glu Glu Met Lys Leu Val Asp Ser Lys
40 15 20 25 30
41 cat ggt cag ctc atc aag aat ttt aca ata cta caa ggt cca ccg ggc 807
42 His Gly Gln Leu Ile Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro Gly
43 35 40 45
44 ccc agg ggt cca aga ggt gac aga gga tcc cag gga ccc cct ggc cca 855
45 Pro Arg Gly Pro Arg Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly Pro
46 50 55 60
47 act ggc aac aag gga cag aaa gga gag aag ggg gag cct gga cca cct 903
48 Thr Gly Asn Lys Gly Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro Pro
49 65 70 75
50 ggc cct gcg ggt gag aga ggc cca att gga cca gct ggt ccc ccc gga 951
51 Gly Pro Ala Gly Glu Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro Gly
52 80 85 90
53 gag cgt ggc ggc aaa gga tct aaa ggc tcc cag ggc ccc aaa ggc tcc 999
54 Glu Arg Gly Gly Lys Gly Ser Lys Gly Ser Gln Gly Pro Lys Gly Ser

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55	95				100					105					110	
56	cgt	ggt	tcc	cct	ggg	aag	ccc	ggc	cct	cag	ggc	ccc	agt	ggg	gac	cca
57	Arg	Gly	Ser	Pro	Gly	Lys	Pro	Gly	Pro	Gln	Gly	Pro	Ser	Gly	Asp	Pro
58					115					120					125	
59	ggc	ccc	ccg	ggc	cca	cca	ggc	aaa	gag	gga	ctc	ccc	ggc	cct	cag	ggc
60	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Lys	Glu	Gly	Leu	Pro	Gly	Pro	Gln	Gly
61					130					135					140	
62	cct	cct	ggc	ttc	cag	gga	ctt	cag	ggc	acc	gtt	ggg	gag	cct	ggg	gtg
63	Pro	Pro	Gly	Phe	Gln	Gly	Leu	Gln	Gly	Thr	Val	Gly	Glu	Pro	Gly	Val
64					145					150					155	
65	cct	gga	cct	cgg	gga	ctg	cca	ggc	ttg	cct	ggg	gta	cca	ggc	atg	cca
66	Pro	Gly	Pro	Arg	Gly	Leu	Pro	Gly	Leu	Pro	Gly	Val	Pro	Gly	Met	Pro
67					160					165					170	
68	ggc	ccc	aag	ggc	ccc	ccc	ggc	cct	cct	ggc	cca	tca	gga	gcg	gtg	gtg
69	Gly	Pro	Lys	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Ser	Gly	Ala	Val	Val
70	175					180					185				190	
71	ccc	ctg	gcc	ctg	cag	aat	gag	cca	acc	ccg	gca	ccg	gag	gac	aat	ggc
72	Pro	Leu	Ala	Leu	Gln	Asn	Glu	Pro	Thr	Pro	Ala	Pro	Glu	Asp	Asn	Gly
73					195					200					205	
74	tgc	ccg	cct	cac	tgg	aag	aac	ttc	aca	gac	aaa	tgc	tac	tat	ttt	tca
75	Cys	Pro	Pro	His	Trp	Lys	Asn	Phe	Thr	Asp	Lys	Cys	Tyr	Tyr	Phe	Ser
76					210					215					220	
77	gtt	gag	aaa	gaa	att	ttt	gag	gat	gca	aag	ctt	ttc	tgt	gaa	gac	aag
78	Val	Glu	Lys	Glu	Ile	Phe	Glu	Asp	Ala	Lys	Leu	Phe	Cys	Glu	Asp	Lys
79					225					230					235	
80	tct	tca	cat	ctt	gtt	ttc	ata	aac	act	aga	gag	gaa	cag	caa	tgg	ata
81	Ser	Ser	His	Leu	Val	Phe	Ile	Asn	Thr	Arg	Glu	Glu	Gln	Gln	Trp	Ile
82					240					245					250	
83	aaa	aaa	cag	atg	gta	ggg	aga	gag	agc	cac	tgg	atc	ggc	ctc	aca	gac
84	Lys	Lys	Gln	Met	Val	Gly	Arg	Glu	Ser	His	Trp	Ile	Gly	Leu	Thr	Asp
85	255					260				265					270	
86	tca	gag	cgt	gaa	aat	gaa	tgg	aag	tgg	ctg	gat	ggg	aca	tct	cca	gac
87	Ser	Glu	Arg	Glu	Asn	Glu	Trp	Lys	Trp	Leu	Asp	Gly	Thr	Ser	Pro	Asp
88					275					280					285	
89	tac	aaa	aat	tgg	aaa	gct	gga	cag	ccg	gat	aac	tgg	ggt	cat	ggc	cat
90	Tyr	Lys	Asn	Trp	Lys	Ala	Gly	Gln	Pro	Asp	Asn	Trp	Gly	His	Gly	His
91					290					295					300	
92	ggg	cca	gga	gaa	gac	tgt	gct	ggg	ttg	att	tat	gct	ggg	cag	tgg	aac
93	Gly	Pro	Gly	Glu	Asp	Cys	Ala	Gly	Leu	Ile	Tyr	Ala	Gly	Gln	Trp	Asn
94					305					310					315	
95	gat	ttc	caa	tgt	gaa	gac	gtc	aat	aac	ttc	att	tgc	gaa	aaa	gac	agg
96	Asp	Phe	Gln	Cys	Glu	Asp	Val	Asn	Asn	Phe	Ile	Cys	Glu	Lys	Asp	Arg
97					320					325					330	
98	gag	aca	gta	ctg	tca	tct	gca	tta	taacggactg	tgatgggatc	acatgagcaa					1725
99	Glu	Thr	Val	Leu	Ser	Ser	Ala	Leu								
100	335					340										
101	atctttcagct	ctcaaaggca	aaggacactc	ctttctaatt	gcacacctt	ctcatcagat										1785
102	tgaaaaaaaaa	aaaagcactg	aaaaccaatt	actgaaaaaa	aattgacagc	tagtggtttt										1845
103	taccatccgt	cattacccaa	agacttgga	actaaaatgt	tccccagggt	gatatgctga										1905

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104 ttttcattgt gcacatggac tgaatcacat agattctcct ccgtcagtaa ccgtgcgatt 1965

105 atacaaatta tgtcttccaa agtatggaac actccaatca gaaaaagggtt atcatcccg 2024

107 <210> SEQ ID NO: 2

108 <211> LENGTH: 547

109 <212> TYPE: PRT

110 <213> ORGANISM: Homo Sapiens

112 <220> FEATURE:

113 <223> OTHER INFORMATION: Deduced Amino Acid Sequence of Novel Collectin from

Nucleotide

114 Sequence

116 <400> SEQUENCE: 2

117 Met Tyr Ser His Asn Val Val Ile Met Asn Leu Asn Asn Leu Asn Leu

118 1 5 10 15

119 Thr Gln Val Gln Gln Arg Asn Leu Ile Thr Asn Leu Gln Arg Ser Val

120 20 25 30

121 Asp Asp Thr Ser Gln Ala Ile Gln Arg Ile Lys Asn Asp Phe Gln Asn

122 35 40 45

123 Leu Gln Gln Val Phe Leu Gln Ala Lys Lys Asp Thr Asp Trp Leu Lys

124 50 55 60

125 Glu Lys Val Gln Ser Leu Gln Thr Leu Ala Ala Asn Asn Ser Ala Leu

126 65 70 75 80

127 Ala Lys Ala Asn Asn Asp Thr Leu Glu Asp Met Asn Ser Gln Leu Asn

128 85 90 95

129 Ser Phe Thr Gly Gln Met Glu Asn Ile Thr Thr Ile Ser Gln Ala Asn

130 100 105 110

131 Glu Gln Asn Leu Lys Asp Leu Gln Asp Leu His Lys Asp Ala Glu Asn

132 115 120 125

133 Arg Thr Ala Ile Lys Phe Asn Gln Leu Glu Glu Arg Phe Gln Leu Phe

134 130 135 140

135 Glu Thr Asp Ile Val Asn Ile Ile Ser Asn Ile Ser Tyr Thr Ala His

136 145 150 155 160

137 His Leu Arg Thr Leu Thr Ser Asn Leu Asn Glu Val Arg Thr Thr Cys

138 165 170 175

139 Thr Asp Thr Leu Thr Lys His Thr Asp Asp Leu Thr Ser Leu Asn Asn

140 180 185 190

141 Thr Leu Ala Asn Ile Arg Leu Asp Ser Val Ser Leu Arg Met Gln Gln

142 195 200 205

143 Asp Leu Met Arg Ser Arg Leu Asp Thr Glu Val Ala Asn Leu Ser Val

144 210 215 220

145 Ile Met Glu Glu Met Lys Leu Val Asp Ser Lys His Gly Gln Leu Ile

146 225 230 235 240

147 Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro Gly Pro Arg Gly Pro Arg

148 245 250 255

149 Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly Pro Thr Gly Asn Lys Gly

150 260 265 270

151 Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Glu

152 275 280 285

153 Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro Gly Glu Arg Gly Gly Lys

154 290 295 300

155 Gly Ser Lys Gly Ser Gln Gly Pro Lys Gly Ser Arg Gly Ser Pro Gly

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156 305          310          315          320
157 Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp Pro Gly Pro Pro Gly Pro
158          325          330          335
159 Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln Gly Pro Pro Gly Phe Gln
160          340          345          350
161 Gly Leu Gln Gly Thr Val Gly Glu Pro Gly Val Pro Gly Pro Arg Gly
162          355          360          365
163 Leu Pro Gly Leu Pro Gly Val Pro Gly Met Pro Gly Pro Lys Gly Pro
164          370          375          380
165 Pro Gly Pro Pro Gly Pro Ser Gly Ala Val Val Pro Leu Ala Leu Gln
166 385          390          395          400
167 Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn Gly Cys Pro Pro His Trp
168          405          410          415
169 Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe Ser Val Glu Lys Glu Ile
170          420          425          430
171 Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp Lys Ser Ser His Leu Val
172          435          440          445
173 Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp Ile Lys Lys Gln Met Val
174          450          455          460
175 Gly Arg Glu Ser His Trp Ile Gly Leu Thr Asp Ser Glu Arg Glu Asn
176 465          470          475          480
177 Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro Asp Tyr Lys Asn Trp Lys
178          485          490          495
179 Ala Gly Gln Pro Asp Asn Trp Gly His Gly His Gly Pro Gly Glu Asp
180          500          505          510
181 Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp Asn Asp Phe Gln Cys Glu
182          515          520          525
183 Asp Val Asn Asn Phe Ile Cys Glu Lys Asp Arg Glu Thr Val Leu Ser
184          530          535          540
185 Ser Ala Leu
186 545

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188 <210> SEQ ID NO: 3

189 <211> LENGTH: 27

190 <212> TYPE: PRT

191 <213> ORGANISM: Artificial Sequence

193 <220> FEATURE:

194 <223> OTHER INFORMATION: Modified Consensus Sequence of collectins Hybridizable with

Novel

195 Collectin

197 <400> SEQUENCE: 3

198 Glu Lys Cys Val Glu Met Tyr Thr Asp Gly Lys Trp Asn Asp Arg Asn

199 1 5 10 15

200 Cys Leu Gln Ser Arg Leu Ala Ile Cys Glu Phe

201 20 25

203 <210> SEQ ID NO: 4

204 <211> LENGTH: 21

205 <212> TYPE: DNA

206 <213> ORGANISM: Artificial Sequence

208 <220> FEATURE:

209 <223> OTHER INFORMATION: Sequence of a Reverse Primer for Screening a Novel

Collectin.

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211 <400> SEQUENCE: 4
 212 caatctgatg agaaggtgat g 21
 214 <210> SEQ ID NO: 5
 215 <211> LENGTH: 21
 216 <212> TYPE: DNA
 217 <213> ORGANISM: Artificial Sequence
 219 <220> FEATURE:
 220 <223> OTHER INFORMATION: Sequence of a Forward Primer for Screening a Novel
 Collectin.
 222 <400> SEQUENCE: 5
 223 acgaggggct ggatgggaca t 21
 225 <210> SEQ ID NO: 6
 226 <211> LENGTH: 27
 227 <212> TYPE: PRT
 228 <213> ORGANISM: Artificial Sequence
 230 <220> FEATURE:
 231 <223> OTHER INFORMATION: Consensus sequence of three collectins which were reported
 232 heretofore
 234 <400> SEQUENCE: 6
 235 Glu Asp Cys Val Leu Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro
 236 1 5 10 15
 237 Cys Ser Thr Ser His Leu Ala Val Cys Glu Phe
 238 20 25
 240 <210> SEQ ID NO: 7
 241 <211> LENGTH: 24
 242 <212> TYPE: DNA
 243 <213> ORGANISM: Artificial Sequence
 245 <220> FEATURE:
 246 <223> OTHER INFORMATION: M13 Universal Primer Sequence for Sequencing
 248 <400> SEQUENCE: 7
 249 cgacgttgta aaacgacggc cagt 24
 251 <210> SEQ ID NO: 8
 252 <211> LENGTH: 17
 253 <212> TYPE: DNA
 254 <213> ORGANISM: Artificial Sequence
 256 <220> FEATURE:
 257 <223> OTHER INFORMATION: M13 Reverse Primer Sequence for Sequencing.
 259 <400> SEQUENCE: 8
 260 caggaaaca gctatgac 17
 262 <210> SEQ ID NO: 9
 263 <211> LENGTH: 24
 264 <212> TYPE: DNA
 265 <213> ORGANISM: Artificial Sequence
 267 <220> FEATURE:
 268 <223> OTHER INFORMATION: Sequence of a lambda gtl1 Reverse Primer for Sequencing.
 270 <400> SEQUENCE: 9
 271 ttgacaccag accaactggt aatg 24
 273 <210> SEQ ID NO: 10
 274 <211> LENGTH: 24
 275 <212> TYPE: DNA

VERIFICATION SUMMARY

DATE: 07/05/2001

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TIME: 10:42:52

Input Set : A:\37157SEQ.txt

Output Set: N:\CRF3\07052001\I763712A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date